CLUSTAL W (1.82) Multiple Sequence Alignments

```
SEQ ID NO:2:      2_HuPS1           467 aa
SEQ ID NO:134:    134_HuPS1         467 aa
SEQ ID NO:4:      4_MuPS1           461 aa


Sequences (2:134)       Aligned. Score:   99
Sequences (2:4)         Aligned. Score:   89
Sequences (134:4)       Aligned. Score:   89
```


```
2_HuPS1        MTELPAPLSYFQNAQMSEDNHLSNTVRSQNDNRERQEHNDRRSLGHPEPLSNGRPQGNSR 60
134_HuPS1      MTELPAPLSYFQNAQMSEDNHLSNTVRSQNDNRERQEHNDRRSLGHPEPLSNGRPQGNSR 60
4_MuPS1        MTEIPAPLSYFQNAQMSEDSHSSSAIRSQNDSQERQQQHDRQRLDNPEPISNGRPQSNSR 60
               ***:************** * * .::***** .:*** ::**: * .:*** ****** ***

2_HuPS1        QVVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTE 120
134_HuPS1      QVVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTE 120
4_MuPS1        QVVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTE 120
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2_HuPS1        DTETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFI 180
134_HuPS1      DTETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFI 180
4_MuPS1        DTETVGQRALHSILNAAIMISVIVIMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFI 180
               ************************:***********************************

2_HuPS1        YLGEVFKTYNVAVDYITVALLIWNLGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKY 240
134_HuPS1      YLGEVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKY 240
4_MuPS1        YLGEVFKTYNV-VDYVTVALLIWNWGVVGMIAIHWKGPLRLQQAYLIMISALMALVFIKY 239
               *********** ***:******** ******:***************************

2_HuPS1        LPEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMAE 300
134_HuPS1      LPEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMAE 300
4_MuPS1        LPEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMAE 299
               ***********************************************************

2_HuPS1        GDPEAQRRVSKNSKYNAESTERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAA 360
134_HuPS1      GDPEAQRRVSKNSKYNAESTERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAA 360
4_MuPS1        GDPEAQRRVPKNPKYNTQRAERETQDSGSGNDDGGFSEEWEAQRDSHLGPHRSTPESRAA 359
               *********.**.***:: :***.**: : ******************************

2_HuPS1        VQELSSSILAGEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILIGLCL 420
134_HuPS1      VQELSSSILAGEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILIGLCL 420
4_MuPS1        VQELSGSILTSEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTTIAC-VAILIGLCL 418
               *****.***:.************************************** *********

2_HuPS1        TLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 467
134_HuPS1      TLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 467
4_MuPS1        -LLLLAIYKKGP--APISITFGFVF-FATDYLVQPFMDQLAFHQFYI 461
               ******:**.     ******:** *******************
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